

MSRRPWLLALALAVALAAGSAGASTGSDATPVATQDGPDY
VFHRAHERMLFQTSYTLENNGSVICIPNNGQCFCLAWLKSNG
TNAEKLAANILQWITFALSALCLMFYGYQTWKSTCGWEEIYVA
TIEMIKFIIEYFHEFDEPAVIYSSNGNKTWLRYAEWLLTCPVILI
HLSNLTGLANDYNKRTMGLLSDIGTIVWGTTAALSKGYVRVI
FFLMGLCYGIYTFFNAAKVYIEAYHTVPKGICRDLVRYLAWLY
FCSWAMFPVLFLGPEGFGHINQFNSAIAHAILDLASKNAWS
MMGHFLRVKIHEHILLYGDIRKKQKVNVAGQEMEVETMVHEE
DDETQKVPTAKYANRDSFIIMRDRLKEKGFETRASLDGDPNG
DAEAAAAGGKPGMEMGKMTGMGMGMGAGMGMAIDS
VILAVPDISMVDFFREQFARLPVYELVPALGAENTLQLVQQA
QSLGGCDFVLMHPEFLRDRSPTGLPRLKMGGQRAAAFGW
AAIGPMRDLIEGSGVDGWLEGPSFGAGINQQALVALINRMQQ
AKKMGMMGGGMGMGGGMGMGMGMGMGMAPSMNAGM
TGGMGGASMGGAVMGMGMGMQMQQAMPAMSPMMTQQ
PSMMSQPSAMSAGGAMQAMGGVMPSPAPGGRVGTNPLFG
SAPSPLSSQPGISPGMATPPAATAAPAAGGSEAEMLQQQLMS
EINRLKNELGE (SEQ ID N°:1)

Fig. 1A

MDYGGALSAVGRELLFVTNPVVNGSVLVPEDQCYCAGWIE
SRGTNGAQTAASNVLQWLAAAGFSILLMFYAYQTWKSTCGWE
EIYVCAIEMVKVILEFFFKNPSMLYLATGHRVQWLRYAEWL
LTCPVILIHLNSNLTGLSNDYSRRTMGLLVSDIGTIWWGATSAMA
TGYVKVIFFCLGLCYGANTFFHAAKAYIEGYHTVPKGRCRQV
VTGMAWLFFVSWGMFPILFILGPEGFGVLSVYGSTVGHTIIDL
MSKNCWGLLGHYLRVLIHEHILIHGDIRKTTKLNIGGTEIEVETL
VEDEAEAGAVNKGTGKYASRESFLVMRDKMKEKGIDVRASL
DNSKEVEQEQAARAAMMMMNNGMGMGMGMNGMNGMG
GMNGMAGGAKPGLELTPQLQPGRVILA VPDISMVDFFREQFA
QLSVTYELVPALGADNTLALVTQAQNLLGGVDFVLIHPEFLRDR
SSTSILSRLRGAGQRVAAGFWAQLGPMRD LIESANLDGWLE
GPSFGQGILPAHIVALVAKMQQMRKMQQQIGMMTGGMN
GMGGGMGGMNGGGNGMNNMGGNGMAGNGMGGGMGGNGMGG
NGMNGMGGNGMNNMGGNGMAGNGMGGGMGGNGMGG
SMNGMSSGVANVTPSAAGGMGGMMNGMAAPQSPGMN
GGRLGTNPLFNAAPSPLSQLGAEAGMGSMMGGMSGM
GGMGGMGGMGGAGAATTQAAGGNAEAEMLQNL MNEINRL
KRELGE (SEQ ID N°:2)

Fig 1B

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MiptavegvsqAQITGRPEWIWLALGTALMGLGTLYFLVKGMGVSDPDAKKFYAITTLVPAIAFTMYLSMLLGYGLTMVPFGGEQNPIYWARYADWLFTTPLLLLALLVDADQGTILALVGADGIMIGTGLVGALTkvSYRFVWWAISTAAMLYILYVLFFGFTSKAESMRPEVASTFKVLRNVTWLWSAYPVWNLIGSEGAGIVPLNIETLLFMVLDVSAKVGFGILLRSRAIFGEAEAPEPSAGDGAAATSD
(SEQ ID NO: 3)

Fig. 1C

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Chop1.	MSRRPWLLALALAVALAAGSAGASTGS	DATAV	PVATQDG	GPDYVFHRA	HERMIFQTSY	TLEN	60		
Chop2.	MDYGGALS	AVGREILFVTNPVVV	23		
Bop.	M		
			*						
Chop1.	NGSYICINNGCFCFLAWLKS	N--	CNAEKKI	ANILQITFALSA	CIMMYCOT	ESTC	118		
Chop2.	NGSIL-VIED-	OCYCA	GATIESR-	-STINGAQTSIV	ONLAACES	ILINNSA	OTK	79	
Bop.	..LPTAVEGVSSQAI	ITGRPEW	WMLA	GTAIMG	GTLYFLVKGM	VSDPDAKKEFYAI	ITLVPA	51	
			*	*	*	*	*		
Chop1.	GMEETAT	EYTHDE	AVI	SSN	IKTV	EE	SNE	178	
Chop2.	GMEETCAT	EVKVL	FIE	TKNSML	PLATCHR	QVQE	EE	139	
Bop.	IAFTMY	--LSH	LLGYGLTMVP	GGEQ	--	--	PIYMAR	D	
			*	*	*	*	*		
Chop1.	ITANDNKET	IN	ESTTAA	SEY	Y	LTME	CTTENAA	IV	235
Chop2.	FISHSR	EDT	TA	MA	Y	CL	CANTEHAA	KA	196
Bop.	V-DA	-Q-G	TEILAVGA	GIMI	GTILVG	TV	SYFVWWAISTAA	MLILYVLF	157
			*	*	*	*	*	*	

Fig. 1D

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Chop1.	<u>TEAHTTPEGICEDLRY</u>	<u>YCSWAN</u>	<u>SPVTT</u>	<u>TIGE</u>	<u>CHINQFNSAIA</u>	<u>AID</u>	295
Chop2.	<u>TEG</u>	<u>HIVEKGRCEQV</u>	<u>TGM</u>	<u>DFIVVNGT</u>	<u>T</u>	<u>T</u>	256
Bop.	<u>SK</u>	<u>ESMREEV</u>	<u>--ASTTEFKV</u>	<u>TRNVTVVLWSAY</u>	<u>VW</u>	<u>ISE</u>	215
	*	*	*	*	*	*	
	#						
Chop1.	<u>SMMG</u>	<u>FIRVK</u>	<u>THEN</u>	<u>LYCDTPPKQ</u>	<u>VV</u>	<u>QMEYETM</u>	354
Chop2.	<u>KNC</u>	<u>GLICH</u>	<u>VIRVLL</u>	<u>LHEDTRTT</u>	<u>NIGHT</u>	<u>HEDETQKVP-TART</u>	316
Bop.	<u>KVG</u>	<u>GLI</u>	<u>--LISRAIFGEAE</u>	<u>PEPSAGDGA-A</u>	<u>TSD</u>	<u>(SEQ ID No: 3)</u>	
	*	*	*	*	*	*	
Chop1.	<u>ANTD</u>	<u>DLTIR</u>	<u>RILK</u>	<u>FEETRASL</u>	<u>GDPNGDATANAA</u>	<u>GGKPGMEMAKMT</u>	414
Chop2.	<u>ASRE</u>	<u>SLV</u>	<u>YV</u>	<u>ERIKMKER</u>	<u>NSKEVEQIQAAR</u>	<u>AMMMNGNCMGMCNNGMNGCN</u>	376
	*	*	*	*	*	*	
Chop1.	<u>SMATIDS</u>	<u>-----</u>	<u>-----</u>	<u>-----</u>	<u>GPVYELVYPAE</u>	<u>GPVYELVYPAE</u>	459
Chop2.	<u>CGMNGMAGGAKPGL</u>	<u>ELTPQLQPRV</u>	<u>IAVED</u>	<u>DESVMYDE</u>	<u>TAQIS</u>	<u>YELVYPAE</u>	436
	*	*	*	*	*	*	
Chop1.	<u>EQVOCAC</u>	<u>SLGGC</u>	<u>DPEVLM</u>	<u>PEPDRSPTGL</u>	<u>PR</u>	<u>KMGCQAZAZ</u>	519
Chop2.	<u>TAAT</u>	<u>TCAQN</u>	<u>LGVD</u>	<u>EVLT</u>	<u>SSISI</u>	<u>AIQPMRDT</u>	496
	*	*	*	*	*	*	
Chop1.	<u>GVDENLEGSE</u>	<u>GAC</u>	<u>INQQALV</u>	<u>AIINRNGQAK</u>	<u>GM</u>	<u>G-----</u>	568
Chop2.	<u>NI</u>	<u>DNLEEE</u>	<u>SEGO</u>	<u>PAHIV</u>	<u>Q</u>	<u>GMMSYCGNG</u>	556

Fig. 1D (continued)

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Chop1 . . CMG-MNG-NAPSNNACM-TGCGC---ASNCG-----AVM SPM 616
 Chop2 . . GGN-NANNINGNGNNGGGTGNLIGNGMNNGCAGNGNNMGMNAGNGGGG GNGNG GGS 616

Chop1 . . MTQQQPS-MMSQPSAMSPPGAMQAMGVMPSAP---SGRVETNPPIEGSKESPRESSO--- 667
 Chop2 . . MNGMSSGVVANVTPSAAGGMMGMAEGRILITNPPIINAKESPSSOLGA 676

(SEQ ID NO.:1) Chop1 . . -----PGLISPQMATPPAATAAPAAGSIAENQQQLMSSEENRIN-TRIGERK 712
 (SEQ ID NO.2) Chop2 . . EAGMGSMGGMGGMSGMGGMGGAGATIQAGENAAEMQNLMNTEENRERGE 737

Fig. 1D (continued)

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....5...10....5...20....5...30....5...40
MDYGGALSAVGRELLFVTNPVVVNGSVLVPEDQCYCAGWI 40
ESRGTNQGAQTASNVLQWLAAAGFSILLLMFYAYQTWKSTCG 80
WEEIYVCAIEMVKVILEFFFFFKNPSMLYLATGHRVQWLR 120
YAEWLLTCPVILIRLSNLTGLSNDYSRRTMGLLVSDIGTI 160
VWGATSAMATGYVKVIFFCCLGLCYGANTFFHAAKAYIEGY 200
HTVPKGRCRQVVTGMAWLFFVSWGMFPILFILGPEGFGVL 240
SVYGSTVGHTIIDLMSKNCWGLLGHYLRVLIHEHILIHD 280
IRKTTKLNIGGTEIEVETLVEDAEAGAVNKGTGK (SEQ ID NO: 4) 315

Fig. 1E